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Minimum DB
Maximum DB
                                                                                                                                                                                              Database
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Perfect score:
                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match
                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                             seg length: 0 seg length: 2000000000
                                                                                                PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 195891 seqs, 67900655 residues
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252
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17.898 Million cell updates/sec
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## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	_	No.	Result	
54	54	54	4.	54.5	4.					55	55	57	57	57	57		58		63	64	67	67	67	67.5	70.5	72	77.5		Score		
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oantiger	in A-typ	D1 - zek	۲.	etical	_	ത	hypothetical prote	heat shock protein	hypothetical prote	rifin PFB1015w - m	oprotein ph	inclusion	inclusion	A-type inclusion p	G		$\leftarrow$	variant-specific s	62K sucrose-bindin	GTPase activating-	thrombospondin 1 p	spondin	protein PV100 [imp	œ.	S	ָ לי	-globulin	alpha-globulin typ	· 5		

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
52	52.5	52.5	52.5	52.5	52.5	52.5	53	53	53	53	53	53.5	53.5	53.5	54
20.6	20.8	20.8	20.8	20.8	20.8	20.8	21.0	21.0	21.0	21.0	21.0	21.2	21.2	21.2	21.4
33	1172	600	425	275	96	91	795	702	702	702	622	1642	301	67	880
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A41822	TSHUP2	T1.8593	T18592	<b>В81430</b>	XLHOA	S00219	I50255	T28570	в72167	S46854	E69006	T08880	I54209	T15592	F75103
antimicrobial pept	thrombospondin 2 p	hypothetical prote	hypothetical prote	probable prephenat	colipase A precurs	ubiquinolcytochr	108K heat shock pr	hypothetical prote	A29L protein - var	A28L protein - var	glutamate synthase	NMDA receptor-bind	hypothetical prote	hypothetical prote	probable purine NT

## ALIGNMENTS

A;Cross references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375
A;Experimental source: var. Coker 201
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533.546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination.
A;Reference number: S06398
A;Accession: S06911
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-81 <CH2>
C;Comment: This is a seed storage protein. alpha-globulin B precursor (clone C72) - upland cotton N;Alternate names: seed storage protein; vicilin precursor C:Species: Gossyplum hirsutum (upland cotton) C:Date: 30-Sep-1991 \*sequence\_revision 30-Sep-1991 \*text\_change 16-Jul-1999 C;Accession: A30838; S06911 R:Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L. Plant Mol. Biol. 7, 475-489, 1986 A;Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N.Alternate names: seed storage protein
C.Species: Gossyplum hirsutum (upland cotton)
C.Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 30-Sep-1993
C.Accession: S08059
R.Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A.Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.
A.Reference number: S06398
A.Accession: S08059
A.Status: not compared with conceptual translation
A.Molecula type. Name DЪ A; Molecule type: DNA A; Residues: 1-509 <CHL> C; Superfamily: glycinin A; Molecule type: mRNA A; Residues: 1-588 < CHL> A; Reference number: A30838 A; Accession: A30838 Matches Query Match 30.8%; Best Local Similarity 41.2%; 3 QRRYEECQQECRQQE-ERQQPQCQQRCLKRFEQE 5 RQEYEECKROCMOLETSGOMRRCVSQCDKRFEED 38 Conservative Score 77.5; DB Pred. No. 0.11; 9; Mismatches 35 2 10; Length 509; Indels 1; Gaps

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R;MCHenry, L.; Fritz, P.J.

Plant Mol. Biol. 18, 1173-1176, 1992

A;Title: Comparison of the structure and nucleotide sequence
A;Reference number: S22477; MUID:92288309

A;Accession: S22477

A;Accession: S22477
                                                                  A:Introns: 211/1; 269/3; 296/3; 391/3; 502/1 C;Superfamily: glyclnin C;Keywords: seed; storage protein F;1-24/Domain: signal sequence #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                               C;Species: Theobroma cacao (cacao)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: S22477; S22478; S18105; S22050
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F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha-globulin type A precursor - upland cotton N,Alternate names: seed storage protein C;Species: Gossypium hirsutum (upland cotton) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change C;Accession: S06398
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C;Keywords: glycoprotein; seed; storage protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #status predicted <MAT>
F;417/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                         C; Genetics:
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A; Residues: 1-452 <MC2>
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A; Residues: 1-566 < MCH>
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A; Title: Development
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A; Residues: 1-605 < CHL>
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9; Mismatches
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A; Molecule type: mRNA
A; Residues: 1-1170 <LAW>
                                  A; Reference number: A26155;
A; Accession: A26155
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A; Residues: 1-810 < YAM>
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J. Blol. Chem. 274, 2563-2570, 1999
A;Title: Multiple functional proteins are produced by cleaving Asn-Gl A; Reference number: 222767; MUID:99107919
A; Accession: 744430
A; Status: prolation
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1987 #sequence_revision
C;Accession: A26155; A34274; A30140; A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein PV100 [imported] - winter squash
C:Species: Cucurbita maxima (winter squash)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: seed C;Comment: This protein is a storage protein which provides nitrogen F;12-33,16-29/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Kimura, M.; Park, S.S.; Sakai, R.; Yamasaki, N.; Funatsu, G. Biosci. Biotechnol. Biochem. 61, 984-988, 1997
A;Title: Primary structure of 6.5k-arginine/glutamate-rich polypeptide A;Reference number: JC5557; MUID:97357433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arginine/glutamate-rich 6.5K polypeptide - smooth loofah C:Species: Luffa cylindrica (smooth loofah) C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1;
                                                                                                                                                              thrombospondin 1 precursor - human
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                                                                                                                                                                                                                                                                     75 RAEYEVCRLRCQVAERGVEQQRKCEQVCEERLREREQGRGEDVD 118
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41.2%;
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                                                                                                                                                                                                                                                                                                                                                                               Score 67; DB Pred. No. 2.8;
                                                                                              on 03-Aug-1995 #text_change 13-Aug-1999
A25812; A05172; A42927
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                                an adhesive glycoprotein with multipl
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C; Function: participates in cell migration and adhesion, and in platelet aggregation A; Description: participates in cell migration and adhesion, and in platelet aggregation C; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vc C; Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer F; 1-18/Domain: signal sequence #status predicted <SIG> F; 19-1170/Product: thrombospondin 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                           F:317-375/Domain: von Willebrand factor type C repeat homology F:378-429/Domain: thrombospondin type 1 repeat homology <THR1> F:434-490/Domain: thrombospondin type 1 repeat homology <THR2> F:491-547/Domain: thrombospondin type 1 repeat homology <THR3> F:551-586/Domain: EGF homology <EGF1>
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A;Accession: A25812
A;Molecule type: mRNA
A;Residues: 1-83; A', 85-397 <KOB>
A;Residues: 1-83; A', 85-397 <KOB>
A;Cross-references: GB:M25631; NID:9538353; PIDN:AAA36741.1; PID:9538354
A;Cross-references: GB:M25631; NID:9538353; PIDN:AAA36741.1; PID:9538354
B;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
                                                                                                                                                                                                                                                                                                                     F:551-586/Domain: EGF homology <EGF1>
F:650-689/Domain: EGF homology <EGF>
F:926-928/Region: cell attachment (R-G-D) motif
F:171-232/Disulfide bonds: #status predicted
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A.Cross-references: GDB:120438; OMIM:188060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Disulfides modulate RGD-inhibitable A;Reference number: A42927; MUID:92348511 A;Accession: A42927 A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: GB:M14326; NID:q340005; PIDN:AAA61237.1; PID:q553801 A:Note: parts of this sequence, including the amino end of the mature pr R:Sun, X.; Skorstengaard, K.; Mosher, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-83,'A',85-522,'A',524-1170 <HEN>
A;Residues: 1-83,'A',BE-522,'A',524-1170 <HEN>
A;Cross-references: EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID:g37465
A;Cross-references: EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID:g37465
A;Note: parts of this sequence, including the amino end of the mature pro
R;Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
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A;Cross-references: GB.J04835
A;Cross-references: GB.J04835
R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotw J. Cell Biol. 108, 729-736, 1989
J. Cell Biol. 108, 729-736, 1989
J. Title: Complete thrombospondin mRNA sequence includes potential regulatory sites A;Reference number: A30140; MUID:89139590
A;Accession: A30140
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A;Note: parts of this sequence, including the amino end of the mature protein, were deterable to the control of the mature protein, were deterable to the control of the mature protein, were deterable to the control of the mature protein, were deterable to the control of the promoter region of the human thrombospondin gene. DNA saccession: A34274; MUID:89291870
A;Accession: A34274
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A; Residues: 1-83, 'A', 85-374, 'RC' <DIX>
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       Query Match
Best Local S
Matches 15
                                                                                                                                                                           270,274/Disulfide bonds: interchain *status predicted 610/Modified site: erythro-beta-hydroxyasparagine (Asn) *status 1051/Binding site: carbohydrate (Asn) (covalent) *status absent
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Cell Biol. 118, 693-701, 1992
                                                                                                                                                                                                                                                                             360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
       Local Similarity hes 15; Conserv
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A; Rotecuar J.F. (LAW)
A; Residues: 1-1170 < LAW)
A; Cross-references: GB:M62449; GB:M62450; GB:M62451; GB:M62470; I
A; Cross-references: GB:M62467; GB:M62468; GB:M62469; GB:M62470; I
M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; I
R; Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P.
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R; Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P.
R; Bornstein, P.; Alfi, P.; Devarayalu, S.; Framson, P.; Li, P.
R; Bornstein, P.; Li, P. (Li, P.)
R; Bornstein, P. (Li, P
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A; Residues: 19-26, 'X', 28-37 < CHE>
C; Complex: homotrimer, disulfide linked
C; Superfamily: thrombospondin 1: EGF homology; thrombospondin
C; Keywords: calcium binding; glycoprotein; homotrimer
F; 1-18, Domain: signal sequence # status predicted < SIG>
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F;491-547/Domain:
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A; Accession: S68787
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A; Residues: 1-1152, 'P', 1154-1170 <LAH>
A; Cross-references: GB: M87276
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A;Molecule type: DNA
A;Residues: 1-490 <BOR>
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A;Title: Characterization of the mouse thrombospondin gene and A;Reference number: A37905; MUID:90375546
A;Accession: A37905
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A; Title: Characterization of the murine thrombospondin A; Reference number: A40558; MUID:92128941
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RSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHW
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                                                                                                                                                                                                                                                      l Similarity
15; Conser
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                            26.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                Score 67; DB Pred. No. 3.9; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.;
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3.9;
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NID:g511867; PIDN:AAA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <VWC>
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protein

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Arabidopsis thaliana

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N;Alternate names: erythrocyte membrane binding protein 1 (EMP1)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: sugar transport
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-524/Product: 62K sucrose-binding protein #status predicted
A; Molecule type: DNA
A; Residues: 1-3078 <
A; Cross-references:
                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                              A;Title: The large diverse gene family var encodes proteins involved in cytoadherence an A;Reference number: Z20487; MUID:95330813
A;Accession: T28432
                                                                                                                                                                R;Su, X.Z.; Heatwole, V.M.; Werthelmer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson, Cell 82, 89-100, 1995
                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                  variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum) N; Alternate names: erythrocyte membrane binding protein 1 (EMP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
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JQ1730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: protein F2K15.210
c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T45840
                                                                                                                                                                                                                                                                                                                                     T28432
                                                                                                                                                                                                                                                                                                                                                                                                                              В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-524 <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: JQ1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Grimes, H.D.; Overvoorde, P.J.; Ripp, K.; Franceschi, V.R.; Hitz, W.D. Plant Cell 4, 1561-574, 1992
A;Title: A 62-kD sucrose binding protein is expressed and localized in ta;Reference number: JQ1730; MUID:93104680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C;Accession: JQ1730
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A; Introns: 53/2; 98/3;
A; Note: F2K15.210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AL132956
A;Experimental source: cultivar Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-554 <RIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62K sucrose-binding protein precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ROEYEECKROCMOLETSGOMRRCVSOCDKRFEEDIDWSK 43
                                                                                                                                                                                                                                                                                                                                                                                                                            EEEDPELVTCKHQCQQQQQYTEGDKRVCLQSCDR 67
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                             <SUX>
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  EMBL:L40608; NID:g886374; PID:g886375; PIDN:AAA75396.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63; DB Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB
Pred. No. 4.5;
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hypothetical protein F6H11.110 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 13-Aug-1999 C;Accession: T05892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Murray, J.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid F31A3.
A;Reference number: 220667
A;Accession: T29699
                                                                                                                 A; Introns: 72/3;
                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1421 <BEV>
A; Cross-references: EMBL: ALO21684
                                                                                                                                                                                                                                                                                              R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; submitted to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: X
A;Introns: 18/3; 160/3
C;Superfamily: ultra-high-sulfur keratin
                                                                                                   A; Note: F6H11.110
                                                                                                                                                            A; Experimental source: cultivar Columbia; C; Genetics:
                                                                                                                                                                                                                                                           A; Reference number: Z15456
A; Accession: T05892
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-242 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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    Matches
                                      Query Match
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Best Local :
                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 AQCEPQCQQSCQQQCVQQQQS--MQQCASACTK 202
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nes 13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SEFDRQEYEECKRQCMQLETSGQMRRCVSQCDK 33
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les 11; Conservative
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                                                                                                                     142/3; 227/2; 344/3;
    Conservative
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                    23.0%;
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    ω
                    Score 58;
Pred. No.
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Pred. No. 70;
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                                                                                                                 1016/3; 1038/3; 1055/1; 1095/2;
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22 GOMRRCVSQCDKRFEEDIDWSKYD 45

GEKRRCLSTTDVTELAEIDWDKID 1111

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A.Status: preliminary
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-586, 'KQ',589-609,'R',611-618,620-682,'S',684-725 <AM2>
A.Residues: 1-586, 'KQ',589-609,'R',611-618,620-682,'S',684-725 <AM2>
A.Cross-references: EMBL:X57318; NID:g62239; PIDN:CAA40574.1; PID:g62241
C:Superfamily: cowpox virus A type inclusion protein
C;Keywords: inclusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A-type inclusion protein - vaccinia virus (strain WR)
C;Species: vaccinia virus
A;Note: host Homo Sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 29-Oct-1999
C;Accession: A41701; A40825; S29908
R;De Carlos, A; Paez, E.
Virology 185, 768-778, 1991
A;Title: Isolation and characterization of mutants of vaccinia virus with a A;Reference number: A41701, MUID:92074241
A;Molecule type: DNA
A;Residues: 1-725 <DEC>
A;Residues: 1-725 <DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, January 1991 A; Reference number: S29907 A; Accession: S29908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross references: GB:M76371; NID:g335683; PIDN:AAA48275.1; PTD:g335684
R;Amegadzie, B.Y.; Sisler, J.R.; Moss, B.
Virology 186, 777-782, 1992
A;Title: Frame-shift mutations within the vaccinia virus A-type inclusion protein gene.
A;Reference number: A40825; MUID:92124754
A;Accession: A40825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14

G71600

rifin PFB1005w - malaria parasite (Plasmodium falciparum)

C;Species: Plasmodium falciparum

C;Species: Plasmodium falciparum

C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000

C;Accession: G71600

R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; K

: Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.;

Science 282, 1126-1132, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-586,'KQ',589-609,'R',611-618,620-682,'S',684-725 <AME>
A;Cross-references: GB:M61187; NID:g335782; PIDN:AAA48321.1; PID:g335784
R;Amegadzie, B.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743 A;Accession: G71600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-316 <GAR>
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Best Local
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                         Local Similarity nes 13; Conserv
                                                 12 KRQCMQLETSGQMRRCVSQCDKRFEEDIDWSK 43
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Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, Ealzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith,
                                                                                                                                              Conservative
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                                                                                                                               11; Mismatches
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Search completed: March 1, 2001, 15:52:28 Job time: 552 sec

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